SEQUENCE LISTING

<110> GUSS, Bengt et al.

<120> IMMUNIZATION OF NON-HUMAN MAMMALS AGAINST STREPTOCOCCUS EQUI

<130> 0825-0173PUS2

<140> US 10/530,879
<141> 2005-04-11

<150> PCT/SE2003/001587
<151> 2003-10-10

<160> 28

<170> PatentIn version 3.1

<210> 1
<211> 180
<212> PRT
<213> Streptococcus equi

<400> 1

Met Ala Leu Asp Ala Thr Thr Val Leu Glu Pro Thr Thr Ala Phe Ile
1 5 10 15

Arg Glu Ala Val Arg Glu Ile Asn Gln Leu Ser Asp Asp Tyr Ala Asp
20 25 30

Asn Gln Glu Leu Gln Ala Val Leu Ala Asn Ala Gly Val Glu Ala Leu
35 40 45

Ala Ala Asp Thr Val Asp Gln Ala Lys Ala Ala Leu Asp Lys Ala Lys
50 55 60

Ala Ala Val Ala Gly Val Gln Leu Asp Glu Ala Arg Arg Glu Ala Tyr
65 70 75 80

Arg Thr Ile Asn Ala Leu Ser Asp Gln His Lys Ser Asp Gln Lys Val
85 90 95

Gln Leu Ala Leu Val Ala Ala Ala Ala Lys Val Ala Asp Ala Ala Ser
100 105 110

Val Asp Gln Val Asn Ala Ala Ile Asn Asp Ala His Thr Ala Ile Ala
115 120 125

BEST AVAILABLE COPY

Asp Ile Thr Gly Ala Ala Leu Leu Glu Ala Lys Glu Ala Ala Ile Asn
130 135 140

Glu Leu Lys Gln Tyr Gly Ile Ser Asp Tyr Tyr Val Thr Leu Ile Asn
145 150 155 160

Lys Ala Lys Thr Val Glu Gly Val Asn Ala Leu Lys Ala Lys Ile Leu
165 170 175

Ser Ala Leu Pro
180

<210> 2
<211> 597
<212> PRT
<213> Streptococcus equi

<400> 2

Met Lys Thr Lys Ser Phe Arg Lys Val Leu Thr Thr Ser Ala Thr Cys
1 5 10 15

Ile Val Leu Ala Thr Ser Phe Ala Gly Gly Thr Leu Arg Val Trp Ala
20 25 30

Glu Gln Leu Tyr Tyr Gly Trp Asn Asp Gly Thr Arg Gln Ser Ser Pro
35 40 45

Tyr Phe Leu Tyr Val Ser Pro Lys Asn Ala Pro Lys Arg Glu Leu Lys
50 55 60

Asp Glu Tyr Val Val Tyr Cys Phe Asn Lys Lys Leu Tyr Trp Pro Asp
65 70 75 80

Gln Trp Glu Ser Ile Tyr Ser Asn Phe Asn Asp Ile Arg Ser Pro Tyr
85 90 95

Asn Asp Leu Pro Val Tyr Glu Lys Lys Leu Gly Tyr Asp Gly Ile Phe
100 105 110

Lys Gln Tyr Ala Pro Asp Tyr Lys Lys Asp Ile Ser Asp Ile Ala Ser
115 120 125

Ala Leu Val Ala Val Leu Ser Asn Gly Tyr Pro Thr Asn Lys Ser Gln
130 135 140

Leu Ser Thr Ser Tyr His Leu Asn Asn Asp Ser Ser Arg Lys Val Thr
145 150 155 160

Gln Leu Ala Ile Trp Tyr Phe Ser Asp Ser Leu Thr Lys Glu Tyr Leu
165 170 175

Lys Asp Thr Gly Gly Tyr Asn Leu Asn Asp Met Glu Lys Lys Ala Leu
180 185 190

Asp Phe Leu Ile Ser Lys Gly Glu Asp Ser Lys Leu Lys Ser Glu Gln
195 200 205

Ser Asn Tyr Ser Leu Asp Ile Tyr Val Tyr Gln Ser Gly Gly His Asp
210 215 220

His Met Lys Asp Tyr Gln Asn Leu Leu Gly Ser Thr Leu Ile Pro Lys
225 230 235 240

Glu Pro Leu Lys Pro Gln Leu Gly Gly Phe Ser Gly His Asn Gly Asn
245 250 255

Gly Leu Ser Gly Leu Glu Gly Gly Ser Ser Gly Ser Gln Glu Thr Asn
260 265 270

Glu Asp Gly Lys Lys Gly Leu Ile Gly Phe His Gly Gly Leu Ser Gly
275 280 285

Ser Glu Gly Lys Arg Asp Pro Leu Pro Gly Leu Lys Gly Glu Ala Gly
290 295 300

Ala Pro Asp Thr Pro Gln Lys Pro Asn Asp Pro Leu Gln Gly Leu Glu
305 310 315 320

Gly Gly Asn Ser Pro Ile Val Glu Gln Asn Tyr Gly Ser Thr Glu Gly
325 330 335

Tyr His Gly Gln Ser Gly Ile Leu Glu Glu Thr Glu Asp Thr Asn Pro
340 345 350

Pro Gly Ile Ile Leu Gly Gly Ser Gly Asn Val Glu Thr His Glu Asp

355 360 365

Thr Arg Asn Pro His Leu Met Gly Ile Gly Gly Gly Leu Ala Gly Glu
370 375 380

Ser Gly Glu Thr Thr Pro Lys Pro Gly Gln Thr Gly Gly Gln Gly Pro
385 390 395 400

Val Ile Glu Thr Thr Glu Asp Thr Gln Lys Gly Met Ser Gly Gln Ser
405 410 415

Gly Gly Thr Ile Glu Ser Glu Asn Thr Lys Lys Pro Glu Val Met Ile
420 425 430

Gly Gly Gln Gly Gln Thr Ile Glu Thr Thr Glu Asp Thr Gln Lys Gly
435 440 445

Met Ser Gly Gln Ser Gly Gly Thr Ile Glu Ser Glu Asp Thr Lys Lys
450 455 460

Pro Glu Val Met Ile Gly Gly Gln Gly Gln Ile Ile Asp Phe Ser Glu
465 470 475 480

Asn Thr Gln Ser Gly Met Ser Gly Gln Ser Gly Asp Thr Thr Val Ile
485 490 495

Glu Asp Thr Lys Lys Ser Glu Ile Ile Ile Gly Gly Gln Gly Gln Ile
500 505 510

Ile Asp Phe Ser Glu Asp Thr Gln Pro Gly Met Ser Gly Gln Ser Gly
515 520 525

Gly Thr Thr Ile Val Glu Asp Thr Lys Lys Pro Thr Pro Lys Pro Lys
530 535 540

Pro Ala Pro Ala Pro Ile Val Asn Asp Glu Lys Pro Asn Lys Gly Thr
545 550 555 560

His Leu Pro Gln Thr Ser Asp Met Lys Gln Leu Thr Leu Ser Ile Ile
565 570 575

Gly Ala Met Ser Met Leu Leu Val Leu Cys Leu Ser Leu Phe Lys Arg
580 585 590

Pro Ser Lys Lys Asp
595

<210> 3
<211> 371
<212> PRT
<213> Streptococcus equi

<400> 3

Met Arg Lys Thr Glu Gly Arg Phe Arg Thr Trp Lys Ser Lys Lys Gln
1 5 10 15

Trp Leu Phe Ala Gly Ala Val Val Thr Ser Leu Leu Leu Gly Ala Ala
20 25 30

Leu Val Phe Gly Gly Leu Leu Gly Ser Leu Gly Gly Ser Ser His Gln
35 40 45

Ala Arg Pro Lys Glu Gln Pro Val Ser Ser Ile Gly Asp Asp Asp Lys
50 55 60

Ser His Lys Ser Ser Ser Asp Ser Met Val Ser Arg Pro Pro Lys Lys
65 70 75 80

Asp Asn Leu Gln Pro Lys Pro Ser Asp Gln Pro Thr Asn His Gln His
85 90 95

Gln Ala Thr Ser Pro Ser Gln Pro Thr Ala Lys Ser Ser Gly His His
100 105 110

Gly Asn Gln Pro Gln Ser Leu Ser Val Asn Ser Gln Gly Asn Ser Ser
115 120 125

Gly Gln Ala Ser Glu Pro Gln Ala Ile Pro Asn Gln Gly Pro Ser Gln
130 135 140

Pro Leu Gly Leu Arg Gly Gly Asn Ser Ser Gly Ser Gly His His His
145 150 155 160

Gln Pro Gln Gly Lys Pro Gln His Leu Asp Leu Gly Lys Asp Asn Ser
165 170 175

Ser Pro Gln Pro Gln Pro Lys Pro Gln Gly Asn Ser Pro Lys Leu Pro
180 185 190

Glu Lys Gly Leu Asn Gly Glu Asn Gln Lys Glu Pro Glu Gln Gly Glu
195 200 205

Arg Gly Glu Ala Gly Pro Pro Leu Ser Gly Leu Ser Gly Asn Asn Gln
210 215 220

Gly Arg Pro Ser Leu Pro Gly Leu Asn Gly Glu Asn Gln Lys Glu Pro
225 230 235 240

Glu Gln Gly Glu Arg Gly Glu Ala Gly Pro Pro Ser Thr Pro Asn Leu
245 250 255

Glu Gly Asn Asn Arg Lys Asn Pro Leu Lys Gly Leu Asp Gly Glu Asn
260 265 270

Lys Pro Lys Glu Asp Leu Asp Gly Lys Gly Leu Ser Gly Glu Asn Asp
275 280 285

Glu Ser Pro Lys Leu Lys Asp Glu His Pro Tyr Asn His Gly Arg Arg
290 295 300

Asp Gly Tyr Arg Val Gly Tyr Glu Asp Gly Tyr Gly Gly Lys Lys His
305 310 315 320

Lys Gly Asp Tyr Pro Lys Arg Phe Asp Glu Ser Ser Pro Lys Glu Tyr
325 330 335

Asn Asp Tyr Ser Gln Gly Tyr Asn Asp Asn Tyr Gly Asn Gly Tyr Leu
340 345 350

Asp Gly Leu Ala Asp Arg Gly Gly Lys Arg Gly Tyr Gly Tyr Ser Tyr
355 360 365

Asn Pro Asp
370

<210> 4
<211> 657
<212> PRT
<213> Streptococcus equi

<400> 4

```
Leu Lys Gln Leu Thr Lys Ile Val Ser Val Val Leu Leu Leu Val Phe
1               5                  10                  15

Thr Leu Ser Ala Ser Leu His Lys Val Arg Ala Thr Asn Leu Ser Asp
            20                  25                  30

Asn Ile Thr Ser Leu Thr Val Ala Ser Ser Ser Leu Arg Asp Gly Glu
        35                  40                  45

Arg Thr Thr Val Lys Val Ala Phe Asp Asp Lys Lys Gln Lys Ile Lys
    50                  55                  60

Ala Gly Asp Thr Ile Glu Val Thr Trp Pro Thr Ser Gly Asn Val Tyr
65                  70                  75                  80

Ile Gln Gly Phe Asn Lys Thr Ile Pro Leu Asn Ile Arg Gly Val Asp
                85                  90                  95

Val Gly Thr Leu Glu Val Thr Leu Asp Lys Ala Val Phe Thr Phe Asn
            100                 105                 110

Gln Asn Ile Glu Thr Met His Asp Val Ser Gly Trp Gly Glu Phe Asp
        115                 120                 125

Ile Thr Val Arg Asn Val Thr Gln Thr Thr Ala Glu Thr Ser Gly Thr
    130                 135                 140

Thr Thr Val Lys Val Gly Asn Arg Thr Ala Thr Ile Thr Val Thr Lys
145                 150                 155                 160

Pro Glu Ala Gly Thr Gly Thr Ser Ser Phe Tyr Tyr Lys Thr Gly Asp
                165                 170                 175

Met Gln Pro Asn Asp Thr Glu Arg Val Arg Trp Phe Leu Leu Ile Asn
            180                 185                 190

Asn Asn Lys Glu Trp Val Ala Asn Thr Val Thr Val Glu Asp Asp Ile
        195                 200                 205

Gln Gly Gly Gln Thr Leu Asp Met Ser Ser Phe Asp Ile Thr Val Ser
    210                 215                 220
```

Gly Tyr Arg Asn Glu Arg Phe Val Gly Glu Asn Ala Leu Thr Glu Phe
225 230 235 240

His Thr Thr Phe Pro Asn Ser Val Ile Thr Ala Thr Asp Asn His Ile
245 250 255

Ser Val Arg Leu Asp Gln Tyr Asp Ala Ser Gln Asn Thr Val Asn Ile
260 265 270

Ala Tyr Lys Thr Lys Ile Thr Asp Phe Asp Gln Lys Glu Phe Ala Asn
275 280 285

Asn Ser Lys Ile Trp Tyr Gln Ile Leu Tyr Lys Asp Gln Val Ser Gly
290 295 300

Gln Glu Ser Asn His Gln Val Ala Asn Ile Asn Ala Asn Gly Gly Val
305 310 315 320

Asp Gly Ser Arg Tyr Thr Ser Phe Thr Val Lys Lys Ile Trp Asn Asp
325 330 335

Lys Glu Asn Gln Asp Gly Lys Arg Pro Lys Thr Ile Thr Val Gln Leu
340 345 350

Tyr Ala Asn Asp Gln Lys Val Asn Asp Lys Thr Ile Glu Leu Ser Asp
355 360 365

Thr Asn Ser Trp Gln Ala Ser Phe Gly Lys Leu Asp Lys Tyr Asp Ser
370 375 380

Gln Asn Gln Lys Ile Thr Tyr Ser Val Lys Glu Val Met Val Pro Val
385 390 395 400

Gly Tyr Gln Ser Gln Val Glu Gly Asp Ser Gly Val Gly Phe Thr Ile
405 410 415

Thr Asn Thr Tyr Thr Pro Glu Val Ile Ser Ile Thr Gly Gln Lys Thr
420 425 430

Trp Asp Asp Arg Glu Asn Gln Asp Gly Lys Arg Pro Lys Glu Ile Thr
435 440 445

Val Arg Leu Leu Ala Asn Asp Ala Ala Thr Asp Lys Val Ala Thr Ala
450 455 460

Ser Glu Gln Thr Gly Trp Lys Tyr Thr Phe Thr Asn Leu Pro Lys Tyr
465 470 475 480

Lys Asp Gly Lys Gln Ile Thr Tyr Thr Ile Gln Glu Asp Pro Val Ala
485 490 495

Asp Tyr Thr Thr Thr Ile Gln Gly Phe Asp Ile Thr Asn His His Glu
500 505 510

Val Ala Leu Thr Ser Leu Lys Val Ile Lys Val Trp Asn Asp Lys Asp
515 520 525

Asp Tyr Tyr His Lys Arg Pro Lys Glu Ile Thr Ile Leu Leu Lys Ala
530 535 540

Asp Gly Lys Val Ile Arg Glu His Gln Met Thr Pro Asp Gln Gln Gly
545 550 555 560

Lys Trp Glu Tyr Thr Phe Asp Gln Leu Pro Val Tyr Gln Thr Gly Lys
565 570 575

Lys Ile Ser Tyr Ser Ile Glu Glu Lys Gln Val Ala Gly Tyr Gln Ala
580 585 590

Pro Val Tyr Glu Val Asp Glu Gly Leu Lys Gln Val Thr Val Thr Asn
595 600 605

Thr Leu Asn Pro Ser Tyr Lys Leu Pro Asp Thr Gly Gly Gln Gly Val
610 615 620

Lys Trp Tyr Leu Leu Ile Gly Gly Gly Phe Ile Ile Val Ala Ile Leu
625 630 635 640

Val Leu Ile Ser Leu Tyr Gln Lys His Lys Arg His Asn Met Ser Lys
645 650 655

Pro

<210> 5

<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> OZAG43B primer used to PCR-amplify a DNA-fragment corresponding to amino acid residues 34-262 in protein EAG

<400> 5
ttttctcgag ctacggtaga gctgataaaa tctc 34

<210> 6
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> OZAG15 primer used to PCR-amplify a DNA-fragment corresponding to amino acid residues 34-262 in protein EAG

<400> 6
tcagccatgg ctctagatgc tacaacggtg tt 32

<210> 7
<211> 600
<212> DNA
<213> Streptococcus equi

<400> 7
aaataatttt gtttaacttt aagaaggaga tataaccatg gctctagatg ctacaacggt 60

gttagagcct acaacagcct tcattagaga agctgttagg gaaatcaatc agctgagtga 120

tgactacgct gacaatcaag agcttcaggc tgttcttgct aatgctggag ttgaggcact 180

tgctgcagat actgttgatc aggctaaagc agctcttgac aaagcaaagg cagctgttgc 240

tggtgttcag cttgatgaag caagacgtga ggcttacaga acaatcaatg ccttaagtga 300

tcagcacaaa agcgatcaaa aggttcagct agctctagtt gctgcagcag ctaaggtggc 360

agatgctgct tcagttgatc aagtgaatgc agccattaat gatgctcata cagctattgc 420

ggacattaca ggagcagcct tgttggaggc taaagaagct gctatcaatg aactaaagca 480

gtatggcatt agtgattact atgtgacctt aatcaacaaa gccaaaactg ttgaaggtgt 540

caatgcgctt aaggcaaaga ttttatcagc tctaccgtag ctcgagcccg ggtgctttgc 600

<210> 8
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> OSFS25 primer used to PCR amplify the 3' end of the sfs gene

<400> 8
ggtcccatgg caactccgaa tttagaagga 30

<210> 9
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> OSFS23 primer used to PCR amplify the 3' end of the sfs gene

<400> 9
cagactcgag gtcgggattg taagaatag 29

<210> 10
<211> 125
<212> PRT
<213> Streptococcus equi

<400> 10

Met Ala Thr Pro Asn Leu Glu Gly Asn Asn Arg Lys Asn Pro Leu Lys
1 5 10 15

Gly Leu Asp Gly Glu Asn Lys Pro Lys Glu Asp Leu Asp Gly Lys Gly
20 25 30

Leu Ser Gly Glu Asn Asp Glu Ser Pro Lys Leu Lys Asp Glu His Pro
35 40 45

Tyr Asn His Gly Arg Arg Asp Gly Tyr Arg Val Gly Tyr Glu Asp Gly
50 55 60

Tyr Gly Gly Lys Lys His Lys Gly Asp Tyr Pro Lys Arg Phe Asp Glu
65 70 75 80

Ser Ser Pro Lys Glu Tyr Asn Asp Tyr Ser Gln Gly Tyr Asn Asp Asn
85 90 95

Tyr Gly Asn Gly Tyr Leu Asp Gly Leu Ala Asp Arg Gly Gly Lys Arg
100 105 110

Gly Tyr Gly Tyr Ser Tyr Asn Pro Asp Leu Glu Pro Gly
115 120 125

<210> 11
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward primer OFNZ1 used to construct the clone pT2fnzN

<400> 11
accatggcta gcgcagagca gctttattat gggt 34

<210> 12
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse primer OFNZ2 used to construct the clone pT2fnzN

<400> 12
atacccggga tatccttcgg tactaccata gt 32

<210> 13
<211> 310
<212> PRT
<213> Streptococcus equi

<400> 13

Met Ala Ser Ala Glu Gln Leu Tyr Tyr Gly Trp Asn Asp Gly Thr Arg
1 5 10 15

Gln Ser Ser Pro Tyr Phe Leu Tyr Val Ser Pro Lys Asn Ala Pro Lys
20 25 30

Arg Glu Leu Lys Asp Glu Tyr Val Val Tyr Cys Phe Asn Lys Lys Leu
35 40 45

Tyr Trp Pro Asp Gln Trp Glu Ser Ile Tyr Ser Asn Phe Asn Asp Ile
50 55 60

Arg Ser Pro Tyr Asn Asp Leu Pro Val Tyr Glu Lys Lys Leu Gly Tyr
65 70 75 80

Asp Gly Ile Phe Lys Gln Tyr Ala Pro Asp Tyr Lys Lys Asp Ile Ser
85 90 95

Asp Ile Ala Ser Ala Leu Val Ala Val Leu Ser Asn Gly Tyr Pro Thr

100 105 110

Asn Lys Ser Gln Leu Ser Thr Ser Tyr His Leu Asn Asn Asp Ser Ser
115 120 125

Arg Lys Val Thr Gln Leu Ala Ile Trp Tyr Phe Ser Asp Ser Leu Thr
130 135 140

Lys Glu Tyr Leu Lys Asp Thr Gly Gly Tyr Asn Leu Asn Asp Met Glu
145 150 155 160

Lys Lys Ala Leu Asp Phe Leu Ile Ser Lys Gly Glu Asp Ser Lys Leu
165 170 175

Lys Ser Glu Gln Ser Asn Tyr Ser Leu Asp Ile Tyr Val Tyr Gln Ser
180 185 190

Gly Gly His Asp His Met Lys Asp Tyr Gln Asn Leu Leu Gly Ser Thr
195 200 205

Leu Ile Pro Lys Glu Pro Leu Lys Pro Gln Leu Gly Gly Phe Ser Gly
210 215 220

His Asn Gly Asn Gly Leu Ser Gly Leu Glu Gly Gly Ser Ser Gly Ser
225 230 235 240

Gln Glu Thr Asn Glu Asp Gly Lys Lys Gly Leu Ile Gly Phe His Gly
245 250 255

Gly Leu Ser Gly Ser Glu Gly Lys Arg Asp Pro Leu Pro Gly Leu Lys
260 265 270

Gly Glu Ala Gly Ala Pro Asp Thr Pro Gln Lys Pro Asn Asp Pro Leu
275 280 285

Gln Gly Leu Glu Gly Gly Asn Ser Pro Ile Val Glu Gln Asn Tyr Gly
290 295 300

Ser Thr Glu Gly Tyr Gly
305 310

<210> 14
<211> 5

<212> PRT
<213> Streptococcus equi

<400> 14
Leu Pro Asp Thr Gly
1 5

<210> 15
<211> 1971
<212> DNA
<213> Streptococcus equi

<400> 15
ttgaaacaac tgacaaagat cgttagtgtg gtcttgttgc tggtctttac ccttagtgct 60

agcctgcaca aggttcgggc aactaatctt agtgacaaca tcacatcatt gacggttgct 120

tcttcatcac tccgagatgg agagagaacg acggtaaagg ttgcgtttga tgacaaaaaa 180

cagaaaatca aggcagggga tacgatagag gtcacctggc ctacaagtgg taatgtctac 240

attcagggct ttaataaaac cataccgctt aatattagag gggtagatgt tggtaccttg 300

gaggtcacgc tagacaaggc tgttttcaca ttcaatcaaa atattgaaac aatgcatgat 360

gtctctggtt ggggagagtt tgatattact gttagaaatg tgacacaaac caccgctgaa 420

acatcaggaa cgaccacagt aaaggtaggc aatcgcactg ctactatcac tgttactaag 480

cctgaggcag gcactggtac cagctcattt tattataaga ctggtgatat gcagcccaat 540

gatactgagc gtgtgagatg gttcctgctg attaacaaca acaaggaatg ggtggccaat 600

actgttacag tcgaagacga tattcaaggt ggtcaaacct tggatatgag cagctttgac 660

atcaccgtat ctggttatcg taacgagcgc ttcgttgggg aaaacgctct gacagagttt 720

catacaacat ttccaaattc tgtcattacg gcaacagata atcacattag tgtgcggtta 780

gatcaatatg atgcctcaca aaacactgtc aacattgctt ataagacaaa gataacggac 840

tttgaccaaa aagaatttgc caacaacagt aaaatctggt accagatttt atacaaggat 900

caggtatcgg gtcaagagtc aaaccaccaa gtagccaata tcaatgctaa cggcggggtt 960

gatggcagtc gctataccag ctttactgtc aagaaaattt ggaatgacaa ggaaaatcaa 1020

gacggtaagc gtccaaagac tattactgtt cagctttacg ccaatgatca gaaagttaat 1080

gataagacca ttgaattgag tgatactaat agctggcaag caagttttgg taagctggat 1140

aagtatgaca gtcagaacca aaaaattacc tacagtgtca aggaagtgat ggttcctgtt 1200

ggctaccaat cgcaggttga gggggatagt ggagtaggat ttaccattac caacacctat 1260

acaccagagg tcattagcat taccggtcaa aaaacttggg acgacaggga aaaccaagac 1320

ggtaaacgtc ctaaggagat tacggttcgt ttattggcaa atgacgctgc aactgacaag 1380

gtagcaactg cttcagagca aaccggctgg aagtatacat ttaccaatct accgaaatac 1440

aaagatggta aacagatcac ctacacgatc caagaggacc ctgtggcaga ttacaccaca 1500

accattcagg gatttgatat taccaatcat catgaggtag ccttgaccag cctaaaggtc 1560

atcaaggttt ggaatgataa ggacgattat taccataaac gtcccaagga gattaccatt 1620

ttgctaaagg cagatggcaa ggtgattcgt gaacatcaga tgacaccgga tcagcaagga 1680

aaatgggaat acacctttga ccagctgccg gtctatcaga caggcaagaa aatcagctac 1740

agcattgagg aaaaacaggt tgctggctat caagcccctg tctatgaggt tgatgaaggc 1800

ttgaagcagg tcactgtaac caacaccctt aacccaagct acaagctgcc tgacaccgga 1860

ggacaaggag tgaaatggta cctgttaatc ggtggcggtt ttatcatcgt cgcaatcctt 1920

gtactgatca gcctttatca aaaacacaag cgccataaca tgtcaaaacc a 1971

<210> 16
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> OSEC1:5 primer used to PCR-amplify a DNA-fragment corresponding to a sequence from amino acid no. 27 to amino acid no. 615 in protein SEC (SEQ. ID. NO: 4)

<400> 16
catgccatgg caactaatct tagtgacaac at 32

<210> 17
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> OSEC3:3 primer used to PCR-amplify a DNA-fragment corresponding to a sequence from amino acid no. 27 to amino acid no. 615 in protein SEC (SEQ. ID. NO: 4)

<400> 17
ccgctcgagc ttgtagcttg ggttaagggt gt 32

<210> 18
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> OSEC2:3 primer used to PCR-amplify a DNA-fragment corresponding to a sequence from amino acid no. 27 to amino acid no. 328 in protein SEC (SEQ. ID. NO: 4)

<400> 18
ccgctcgaga aagctggtat agcgactgcc at 32

<210> 19
<211> 1782
<212> DNA
<213> Streptococcus equi

<400> 19
atggcaacta atcttagtga caacatcaca tcattgacgg ttgcttcttc atcactccga 60

gatggagaga gaacgacggt aaaggttgcg tttgatgaca aaaaacagaa aatcaaggca 120

ggggatacga tagaggtcac ctggcctaca agtggtaatg tctacattca gggctttaat 180

aaaaccatac cgcttaatat tagaggggta gatgttggta ccttggaggt cacgctagac 240

aaggctgttt tcacattcaa tcaaaatatt gaaacaatgc atgatgtctc tggttgggga 300

gagtttgata ttactgttag aaatgtgaca caaaccaccg ctgaaacatc aggaacgacc 360

acagtaaagg taggcaatcg cactgctact atcactgtta ctaagcctga ggcaggcact 420

ggtaccagct cattttatta taagactggt gatattcagc ccaatgatac tgagcgtgtg 480

agatggttcc tgctgattaa caacaacaag gaatgggtgg ccaatactgt tacagtcgaa 540

gacgatattc aaggtggtca aaccttggat atgagcagct ttgacatcac cgtatctggt 600

tatcgtaacg agcgcttcgt tggggaaaac gctctgacag agtttcatac aacatttcca 660

aattctgtca ttacggcaac agataatcac attagtgtgc ggttagatca atatgatgcc 720

tcacaaaaca ctgtcaacat tgcttataag acaaagataa cggactttga ccaaaaagaa 780

tttgccaaca acagtaaaat ctggtaccag attttataca aggatcaggt atcgggtcaa 840

gagtcaaacc accaagtagc caatatcaat gctaacggcg gggttgatgg cagtcgctat 900

accagcttta ctgtcaagaa aatttggaat gacaaggaaa atcaagacgg taagcgtcca 960

aagactatta ctgttcagct ttacgccaat gatcagaaag ttaatgataa gaccattgaa 1020

ttgagtgata ctaatagctg gcaagcaagt tttggtaagc tggataagta tgacagtcag 1080

aaccaaaaaa ttacctacag tgtcaaggaa gtgatggttc ctgttggcta ccaatcgcag 1140

gttgaggggg atagtggagt aggatttacc attaccaaca cctatacacc agaggtcatt 1200

agcattaccg gtcaaaaaac ttgggacgac agggaaaacc aagacggtaa acgtcctaag 1260

gagattacgg ttcgtttatt ggcaaatgac gctgcaactg acaaggtagc aactgcttca 1320

gagcaaaccg gctggaagta tacatttacc aatctaccga aatacaaaga tggtaaacag 1380

atcacctaca cgatccaaga ggaccctgtg gcagattaca ccacaaccat tcagggattt 1440

gatattacca atcatcatga ggtagccttg accagcctaa aggtcatcaa ggtttggaat 1500

gataaggacg attattacca taaacgtccc aaggagatta ccattttgct aaaggcagat 1560

ggcaaggtga ttcgtgaaca tcagatgaca ccggatcagc aaggaaaatg ggaatacacc 1620

tttgaccagc tgccggtcta tcaggcaggc aagaaaatca gctacagcat tgaggaaaaa 1680

caggttgctg gctatcaagc ccctgtctat gaggttgatg aaggcttgaa gcaggtcact 1740

gtaaccaaca cccttaaccc aagctacaag ctcgagcccg gg 1782

<210> 20
<211> 594
<212> PRT
<213> Streptococcus equi

<400> 20

Met Ala Thr Asn Leu Ser Asp Asn Ile Thr Ser Leu Thr Val Ala Ser
1 5 10 15

Ser Ser Leu Arg Asp Gly Glu Arg Thr Thr Val Lys Val Ala Phe Asp
20 25 30

Asp Lys Lys Gln Lys Ile Lys Ala Gly Asp Thr Ile Glu Val Thr Trp
35 40 45

Pro Thr Ser Gly Asn Val Tyr Ile Gln Gly Phe Asn Lys Thr Ile Pro
50 55 60

Leu Asn Ile Arg Gly Val Asp Val Gly Thr Leu Glu Val Thr Leu Asp
65 70 75 80

Lys Ala Val Phe Thr Phe Asn Gln Asn Ile Glu Thr Met His Asp Val
85 90 95

Ser Gly Trp Gly Glu Phe Asp Ile Thr Val Arg Asn Val Thr Gln Thr
100 105 110

Thr Ala Glu Thr Ser Gly Thr Thr Thr Val Lys Val Gly Asn Arg Thr
115 120 125

```
Ala Thr Ile Thr Val Thr Lys Pro Glu Ala Gly Thr Gly Thr Ser Ser
    130                 135                 140

Phe Tyr Tyr Lys Thr Gly Asp Ile Gln Pro Asn Asp Thr Glu Arg Val
145                 150                 155                 160

Arg Trp Phe Leu Leu Ile Asn Asn Asn Lys Glu Trp Val Ala Asn Thr
                165                 170                 175

Val Thr Val Glu Asp Asp Ile Gln Gly Gly Gln Thr Leu Asp Met Ser
            180                 185                 190

Ser Phe Asp Ile Thr Val Ser Gly Tyr Arg Asn Glu Arg Phe Val Gly
        195                 200                 205

Glu Asn Ala Leu Thr Glu Phe His Thr Thr Phe Pro Asn Ser Val Ile
    210                 215                 220

Thr Ala Thr Asp Asn His Ile Ser Val Arg Leu Asp Gln Tyr Asp Ala
225                 230                 235                 240

Ser Gln Asn Thr Val Asn Ile Ala Tyr Lys Thr Lys Ile Thr Asp Phe
                245                 250                 255

Asp Gln Lys Glu Phe Ala Asn Asn Ser Lys Ile Trp Tyr Gln Ile Leu
            260                 265                 270

Tyr Lys Asp Gln Val Ser Gly Gln Glu Ser Asn His Gln Val Ala Asn
        275                 280                 285

Ile Asn Ala Asn Gly Gly Val Asp Gly Ser Arg Tyr Thr Ser Phe Thr
    290                 295                 300

Val Lys Lys Ile Trp Asn Asp Lys Glu Asn Gln Asp Gly Lys Arg Pro
305                 310                 315                 320

Lys Thr Ile Thr Val Gln Leu Tyr Ala Asn Asp Gln Lys Val Asn Asp
                325                 330                 335

Lys Thr Ile Glu Leu Ser Asp Thr Asn Ser Trp Gln Ala Ser Phe Gly
            340                 345                 350
```

Lys Leu Asp Lys Tyr Asp Ser Gln Asn Gln Lys Ile Thr Tyr Ser Val
355 360 365

Lys Glu Val Met Val Pro Val Gly Tyr Gln Ser Gln Val Glu Gly Asp
370 375 380

Ser Gly Val Gly Phe Thr Ile Thr Asn Thr Tyr Thr Pro Glu Val Ile
385 390 395 400

Ser Ile Thr Gly Gln Lys Thr Trp Asp Asp Arg Glu Asn Gln Asp Gly
405 410 415

Lys Arg Pro Lys Glu Ile Thr Val Arg Leu Leu Ala Asn Asp Ala Ala
420 425 430

Thr Asp Lys Val Ala Thr Ala Ser Glu Gln Thr Gly Trp Lys Tyr Thr
435 440 445

Phe Thr Asn Leu Pro Lys Tyr Lys Asp Gly Lys Gln Ile Thr Tyr Thr
450 455 460

Ile Gln Glu Asp Pro Val Ala Asp Tyr Thr Thr Thr Ile Gln Gly Phe
465 470 475 480

Asp Ile Thr Asn His His Glu Val Ala Leu Thr Ser Leu Lys Val Ile
485 490 495

Lys Val Trp Asn Asp Lys Asp Asp Tyr Tyr His Lys Arg Pro Lys Glu
500 505 510

Ile Thr Ile Leu Leu Lys Ala Asp Gly Lys Val Ile Arg Glu His Gln
515 520 525

Met Thr Pro Asp Gln Gln Gly Lys Trp Glu Tyr Thr Phe Asp Gln Leu
530 535 540

Pro Val Tyr Gln Ala Gly Lys Lys Ile Ser Tyr Ser Ile Glu Glu Lys
545 550 555 560

Gln Val Ala Gly Tyr Gln Ala Pro Val Tyr Glu Val Asp Glu Gly Leu
565 570 575

Lys Gln Val Thr Val Thr Asn Thr Leu Asn Pro Ser Tyr Lys Leu Glu

580 585 590

Pro Gly

<210> 21
<211> 921
<212> DNA
<213> Streptococcus equi

<400> 21
atggcaacta atcttagtga caacatcaca tcattgacgg ttgcttcttc atcactccga 60

gatggagaga gaacgacggt aaaggttgcg tttgatgaca aaaaacagaa aatcaaggca 120

ggggatacga tagaggtcac ctggcctaca agtggtaatg tctacattca gggctttaat 180

aaaaccatac cgcttaatat tagaggggta gatgttggta ccttggaggt cacgctagac 240

aaggctgttt tcacattcaa tcaaaatatt gaaacaatgc atgatgtctc tggttgggga 300

gagtttgata ttactgttag aaatgtgaca caaaccaccg ctgaaacatc aggaacgacc 360

acagtaaagg taggcaatcg cactgctact atcactgtta ctaagcctga ggcaggcact 420

ggtaccagct cattttatta taagactggt gatatgcagc ccaatgatac tgagcgtgtg 480

agatggttcc tgctgattaa caacaacaag gaatgggtgg ccaatactgt tacagtcgaa 540

gacgatattc aaggtggtca aaccttggat atgagcagct ttgacatcac cgtatctggt 600

tatcgtaacg agcgcttcgt tggggaaaac gctctgacag agtttcatac aacatttcca 660

aattctgtca ttacggcaac agataatcac attagtgtgc ggttagatca atatgatgcc 720

tcacaaaaca ctgtcaacat tgcttataag acaaagataa cggactttga ccaaaaagaa 780

tttgccaaca acagtaaaat ctggtaccag attttataca aggatcaggt atcgggtcaa 840

gagtcaaacc accaagtagc caatatcaat gctaacggcg gggttgatgg cagtcgctat 900

accagctttc tcgagcccgg g 921

<210> 22
<211> 307
<212> PRT
<213> Streptococcus equi

<400> 22

Met Ala Thr Asn Leu Ser Asp Asn Ile Thr Ser Leu Thr Val Ala Ser
1 5 10 15

```
Ser Ser Leu Arg Asp Gly Glu Arg Thr Thr Val Lys Val Ala Phe Asp
            20                  25                  30

Asp Lys Lys Gln Lys Ile Lys Ala Gly Asp Thr Ile Glu Val Thr Trp
        35                  40                  45

Pro Thr Ser Gly Asn Val Tyr Ile Gln Gly Phe Asn Lys Thr Ile Pro
    50                  55                  60

Leu Asn Ile Arg Gly Val Asp Val Gly Thr Leu Glu Val Thr Leu Asp
65                  70                  75                  80

Lys Ala Val Phe Thr Phe Asn Gln Asn Ile Glu Thr Met His Asp Val
                85                  90                  95

Ser Gly Trp Gly Glu Phe Asp Ile Thr Val Arg Asn Val Thr Gln Thr
            100                 105                 110

Thr Ala Glu Thr Ser Gly Thr Thr Thr Val Lys Val Gly Asn Arg Thr
        115                 120                 125

Ala Thr Ile Thr Val Thr Lys Pro Glu Ala Gly Thr Gly Thr Ser Ser
    130                 135                 140

Phe Tyr Tyr Lys Thr Gly Asp Met Gln Pro Asn Asp Thr Glu Arg Val
145                 150                 155                 160

Arg Trp Phe Leu Leu Ile Asn Asn Asn Lys Glu Trp Val Ala Asn Thr
                165                 170                 175

Val Thr Val Glu Asp Asp Ile Gln Gly Gly Gln Thr Leu Asp Met Ser
            180                 185                 190

Ser Phe Asp Ile Thr Val Ser Gly Tyr Arg Asn Glu Arg Phe Val Gly
        195                 200                 205

Glu Asn Ala Leu Thr Glu Phe His Thr Thr Phe Pro Asn Ser Val Ile
    210                 215                 220

Thr Ala Thr Asp Asn His Ile Ser Val Arg Leu Asp Gln Tyr Asp Ala
225                 230                 235                 240

Ser Gln Asn Thr Val Asn Ile Ala Tyr Lys Thr Lys Ile Thr Asp Phe
```

245 250 255

Asp Gln Lys Glu Phe Ala Asn Asn Ser Lys Ile Trp Tyr Gln Ile Leu
260 265 270

Tyr Lys Asp Gln Val Ser Gly Gln Glu Ser Asn His Gln Val Ala Asn
275 280 285

Ile Asn Ala Asn Gly Gly Val Asp Gly Ser Arg Tyr Thr Ser Phe Leu
290 295 300

Glu Pro Gly
305

<210> 23
<211> 302
<212> PRT
<213> Streptococcus equi

<400> 23

Met Thr Asn Lys Thr Lys Arg Thr Gly Leu Val Arg Lys Tyr Gly Ala
1 5 10 15

Cys Ser Ala Ala Ile Ala Leu Ala Ala Leu Ala Ser Leu Gly Ala Gly
20 25 30

Lys Ala Val Lys Ala Asp Gln Pro Ala Ala Leu Lys Tyr Pro Glu Pro
35 40 45

Arg Asp Tyr Phe Leu His Thr Arg Glu Gly Asp Val Ile Tyr Asp Glu
50 55 60

Asp Ile Lys Arg Tyr Phe Glu Asp Leu Glu Ala Tyr Leu Thr Ala Arg
65 70 75 80

Leu Gly Gly Ile Asp Lys Lys Val Glu Glu Ala Ala Gln Lys Pro Gly
85 90 95

Ile Pro Gly Pro Thr Gly Pro Gln Gly Pro Lys Gly Asp Lys Gly Asp
100 105 110

Pro Gly Ala Pro Gly Glu Arg Gly Pro Ala Gly Pro Lys Gly Asp Thr
115 120 125

```
Gly Glu Ala Gly Pro Arg Gly Glu Gln Gly Pro Ala Gly Gln Ala Gly
    130                 135                 140

Glu Arg Gly Pro Lys Gly Asp Pro Gly Ala Pro Gly Pro Lys Gly Glu
145                 150                 155                 160

Lys Gly Asp Thr Gly Ala Val Gly Pro Lys Gly Glu Lys Gly Asp Thr
                165                 170                 175

Gly Ala Thr Gly Pro Lys Gly Asp Lys Gly Glu Arg Gly Glu Lys Gly
            180                 185                 190

Glu Gln Gly Gln Arg Gly Glu Lys Gly Glu Gln Gly Gln Arg Gly Glu
        195                 200                 205

Lys Gly Glu Gln Lys Pro Lys Gly Asp Gln Gly Lys Asp Thr Lys Pro
    210                 215                 220

Ser Ala Pro Lys Ala Pro Glu Lys Ala Pro Ala Pro Lys Ala Pro Lys
225                 230                 235                 240

Ala Ser Glu Gln Ser Ser Asn Pro Lys Ala Pro Ala Pro Lys Ser Ala
                245                 250                 255

Pro Ser Lys Ser Ala Ala Pro Thr Gly Gln Lys Ala Ala Leu Pro Ala
            260                 265                 270

Thr Gly Glu Ile Asn His Pro Phe Phe Thr Leu Ala Ala Leu Ser Val
        275                 280                 285

Ile Ala Ser Val Gly Val Leu Thr Leu Lys Gly Lys Lys Asp
    290                 295                 300
```

<210> 24
<211> 909
<212> DNA
<213> Streptococcus equi

<400> 24
atgacaaaca aaacaaagcg tacaggattg gtacgcaagt acggtgcctg ctcagcagct 60

atcgccttag cagctcttgc aagcctggga gcaggtaaag cagtaaaggc agaccagcca 120

gcagcactaa aatatccaga acctagagac tattttcttc atactcgtga aggtgatgtt 180

atttatgatg aggatataaa aagatatttt gaggatttag aagcctattt aacagctaga 240

cttggtggga ttgataaaaa agtagaagaa gctgcccaaa agccaggtat tccaggtcct 300

actggccctc aaggtcctaa gggagacaaa ggagatccag gtgcccctgg tgagcgcggt 360

ccagctggac caaagggcga tacgggcgaa gccggaccaa gaggtgagca aggcccagcc 420

ggacaagctg gagaacgtgg accaaaagga gatccaggtg ctccaggtcc taaaggtgaa 480

aagggtgata ctggtgcagt tggtcctaaa ggtgaaaaag gtgataccgg agcaaccgga 540

ccaaagggag acaagggcga acgcggtgaa aaaggcgagc aaggccaacg tggcgaaaaa 600

ggcgagcaag gccaacgcgg tgaaaaaggc gagcaaaaac caaagggtga tcaaggaaaa 660

gatacaaaac catcagctcc aaaagcacct gaaaaggctc ctgcaccaaa agctccaaag 720

gcttcagagc agtcatctaa tcctaaagca ccagctccta agtcagcacc aagcaaatca 780

gcggcaccaa caggtcaaaa agcagcccta ccagcaacag gggaaatcaa ccacccattc 840

ttcacccttg cagctcttag tgtcatcgct agcgtaggcg tcctaactct aaaaggaaaa 900

aaagactaa 909

<210> 25
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> OSCL2:5 primer used to PCR-amplify a DNA-fragment corresponding to amino acid 38 to amino acid 269 in protein SclC

<400> 25
catgccatgg accagccagc agcactaaaa tat 33

<210> 26
<211> 31
<212> DNA
<213> Artificial Sequence

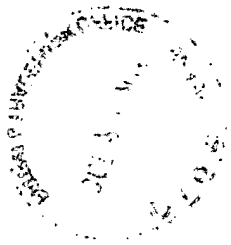
<220>
<223> OSCL3:3 primer used to PCR-amplify a DNA-fragment corresponding to amino acid 38 to amino acid 269 in protein SclC

<400> 26
ccgctcgagg gctgcttttt gacctgttgg t 31

<210> 27
<211> 237
<212> PRT
<213> Streptococcus equi

<400> 27

```
Met Asp Gln Pro Ala Ala Leu Lys Tyr Pro Glu Pro Arg Asp Tyr Phe
1               5                  10                  15

Leu His Thr Arg Glu Gly Asp Val Ile Tyr Asp Glu Asp Ile Lys Arg
            20                  25                  30

Tyr Phe Glu Asp Leu Glu Ala Tyr Leu Thr Ala Arg Leu Gly Gly Ile
        35                  40                  45

Asp Lys Lys Val Glu Glu Ala Ala Gln Lys Pro Gly Ile Pro Gly Pro
    50                  55                  60

Thr Gly Pro Gln Gly Pro Lys Gly Asp Lys Gly Asp Pro Gly Ala Pro
65                  70                  75                  80

Gly Glu Arg Gly Pro Ala Gly Pro Lys Gly Asp Thr Gly Glu Ala Gly
                85                  90                  95

Pro Arg Gly Glu Gln Gly Pro Ala Gly Gln Ala Gly Glu Arg Gly Pro
            100                 105                 110

Lys Gly Asp Pro Gly Ala Pro Gly Pro Lys Gly Glu Lys Gly Asp Thr
        115                 120                 125

Gly Ala Val Gly Pro Lys Gly Glu Lys Gly Asp Thr Gly Ala Thr Gly
    130                 135                 140

Pro Lys Gly Asp Lys Gly Glu Arg Gly Glu Lys Gly Glu Gln Gly Gln
145                 150                 155                 160

Arg Gly Glu Lys Gly Glu Gln Gly Gln Arg Gly Glu Lys Gly Glu Gln
                165                 170                 175

Lys Pro Lys Gly Asp Gln Gly Lys Asp Thr Lys Pro Ser Ala Pro Lys
            180                 185                 190

Ala Pro Glu Lys Ala Pro Ala Pro Lys Ala Pro Lys Ala Ser Glu Gln
        195                 200                 205

Ser Ser Asn Pro Lys Ala Pro Ala Pro Lys Ser Ala Pro Ser Lys Ser
    210                 215                 220
```



Ala Ala Pro Thr Gly Gln Lys Ala Ala Leu Glu Pro Gly
225 230 235

<210> 28
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Motif corresponding to the LPDTG motif (SEQ. ID. NO: 14) of the SEC protein

<220>
<221> misc_feature
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<400> 28

Leu Pro Xaa Thr Gly
1 5

This Page is Inserted by IFW Indexing and Scanning Operations and is not part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☐ FADED TEXT OR DRAWING
- ☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☐ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.
As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.